```
BLASTP 2.2.20+
Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro
A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and
David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new
generation of protein database search programs", Nucleic
Acids Res. 25:3389-3402.


RID: YSWSR5KT01R


Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF excluding environmental samples
from WGS projects
           8,267,994 sequences; 2,848,338,404 total letters
Query=
Length=16
```

```
                                                           Score      E
Sequences producing significant alignments:               (Bits)   Value

gb|AAA30830.1|  apolipoprotein C-III precursor             25.2     0.078
gb|AAA31389.1|  macrophage cationic peptide 2 (MCP-2) >gb|AAA3... 21.8  0.82
gb|AAA40730.1|  amylin precursor >gb|AAA41359.1| islet amyloid... 21.8  0.82
gb|AAA37874.1|  islet amyloid polypeptide                  21.8     0.82
gb|AAA51760.1|  apolipoprotein C-III precursor >gb|AAA51761.1|... 21.8  0.82
gb|AAA31387.1|  macrophage cationic peptide 1 (MCP-1) precurso... 21.8  0.82
gb|AAA30759.1|  seminalplasmin precursor                   21.4     1.1
gb|AAA26479.1|  xis-like gene; putative                    21.0     1.5
gb|AAA18561.1|  putative. similar to phospholipid transfer pro... 21.0  1.5
gb|AAA31236.1|  defensin NP-3a >gb|AAA31237.1| defensin NP-3a 20.6   2.0
```

```
ALIGNMENTS
>gb|AAA30830.1| apolipoprotein C-III precursor
Length=100

 Score = 25.2 bits (52),  Expect = 0.078
 Identities = 9/11 (81%), Positives = 9/11 (81%), Gaps = 0/11 (0%)


Query  5    LLPAVLLALLA  15
            LL A LLALLA
Sbjct  6    LLVAALLALLA  16



>gb|AAA31389.1| macrophage cationic peptide 2 (MCP-2)
 gb|AAA31390.1| macrophage cationic peptide 2 (MCP-2) precursor
 gb|AAA31424.1| corticostatin CS-4
Length=95

 Score = 21.8 bits (44),  Expect = 0.82
 Identities = 9/13 (69%), Positives = 10/13 (76%), Gaps = 1/13 (7%)


Query  4    ALLPAVLL-ALLA  15
            ALL A+LL AL A
Sbjct  5    ALLAAILLVALQA  17


 Score = 17.2 bits (33),  Expect =    21
 Identities = 5/5 (100%), Positives = 5/5 (100%), Gaps = 0/5 (0%)
```

```
Query  11   LALLA   15
            LALLA
Sbjct   4   LALLA   8
```

>gb|AAA40730.1| amylin precursor
 gb|AAA41359.1| islet amyloid polypeptide
Length=93

 Score = 21.8 bits (44), Expect = 0.82
 Identities = 7/8 (87%), Positives = 7/8 (87%), Gaps = 0/8 (0%)

```
Query   6   LPAVLLAL   13
            LPAVLL L
Sbjct   7   LPAVLLIL   14
```

>gb|AAA37874.1| islet amyloid polypeptide
Length=93

 Score = 21.8 bits (44), Expect = 0.82
 Identities = 7/8 (87%), Positives = 7/8 (87%), Gaps = 0/8 (0%)

```
Query   6   LPAVLLAL   13
            LPAVLL L
Sbjct   7   LPAVLLIL   14
```

 Score = 9.1 bits (14), Expect = 5560
 Identities = 2/2 (100%), Positives = 2/2 (100%), Gaps = 0/2 (0%)

```
Query  13   LL   14
            LL
Sbjct  91   LL   92
```

>gb|AAA51760.1| apolipoprotein C-III precursor
 gb|AAA51761.1| apolipoprotein C-III precursor
Length=99

 Score = 21.8 bits (44), Expect = 0.82
 Identities = 8/11 (72%), Positives = 8/11 (72%), Gaps = 0/11 (0%)

```
Query   5   LLPAVLLALLA   15
            LL   LLALLA
Sbjct   6   LLVVALLALLA   16
```

>gb|AAA31387.1| macrophage cationic peptide 1 (MCP-1) precursor
 gb|AAA31388.1| macrophage cationic peptide (MCP-1)
Length=95

 Score = 21.8 bits (44), Expect = 0.82
 Identities = 9/13 (69%), Positives = 10/13 (76%), Gaps = 1/13 (7%)

```
Query   4   ALLPAVLL-ALLA   15
            ALL A+LL AL A
Sbjct   5   ALLAAILLVALQA   17
```

```
 Score = 17.2 bits (33),  Expect =    21
 Identities = 5/5 (100%), Positives = 5/5 (100%), Gaps = 0/5 (0%)


Query  11   LALLA  15
            LALLA
Sbjct   4   LALLA   8



>gb|AAA30759.1| seminalplasmin precursor
Length=80

 Score = 21.4 bits (43),  Expect = 1.1
 Identities = 8/11 (72%), Positives = 8/11 (72%), Gaps = 3/11 (27%)


Query   7   PA---VLLALL  14
            PA   VLLALL
Sbjct   9   PAMATVLLALL  19



>gb|AAA26479.1| xis-like gene; putative
Length=92

 Score = 21.0 bits (42),  Expect = 1.5
 Identities = 10/21 (47%), Positives = 13/21 (61%), Gaps = 6/21 (28%)


Query   1   AAVALL------PAVLLALLA  15
            AAVA+L      P +L+A LA
Sbjct  23   AAVAVLLWRAVLPVILIAALA  43


 Score = 20.2 bits (40),  Expect = 2.7
 Identities = 9/15 (60%), Positives = 10/15 (66%), Gaps = 4/15 (26%)


Query   1   AAVALLPA----VLL  11
            AA+ALL A    VLL
Sbjct  15   AALALLTAAAVAVLL  29


 Score = 18.5 bits (36),  Expect = 8.6
 Identities = 7/9 (77%), Positives = 7/9 (77%), Gaps = 2/9 (22%)


Query   8   AVL--LALL  14
            AVL  LALL
Sbjct  12   AVLAALALL  20


 Score = 15.9 bits (30),  Expect =    50
 Identities = 7/13 (53%), Positives = 10/13 (76%), Gaps = 0/13 (0%)


Query   1   AAVALLPAVLLAL  13
            AA+A L  ++LAL
Sbjct  58   AALAALRGLMLAL  70


 Score = 13.4 bits (24),  Expect =   294
 Identities = 4/5 (80%), Positives = 5/5 (100%), Gaps = 0/5 (0%)


Query  11   LALLA  15
            LA+LA
```

```
Sbjct  11   LAVLA  15


 Score = 12.9 bits (23),  Expect =   394
 Identities = 6/9 (66%), Positives = 6/9 (66%), Gaps = 2/9 (22%)

Query  9   VL--LALLA  15
           VL  LA LA
Sbjct  10  VLAVLAALA  18


>gb|AAA18561.1| putative. similar to phospholipid transfer proteins
Length=29

 Score = 21.0 bits (42),  Expect = 1.5
 Identities = 9/14 (64%), Positives = 11/14 (78%), Gaps = 2/14 (14%)

Query  2   AVALLPAVLLALLA  15
           AVA++ AVL  LLA
Sbjct  9   AVAVVAAVL--LLA  20


>gb|AAA31236.1| defensin NP-3a
 gb|AAA31237.1| defensin NP-3a
Length=93

 Score = 20.6 bits (41),  Expect = 2.0
 Identities = 7/10 (70%), Positives = 8/10 (80%), Gaps = 0/10 (0%)

Query  5   LLPAVLLALL  14
           LL A+LLA L
Sbjct  6   LLAAILLAAL  15



  Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF
excluding environmental samples from WGS projects
    Posted date:  Apr 17, 2009  6:11 PM
  Number of letters in database: 306,907
  Number of sequences in database:  5,031

Lambda     K       H
   0.335   0.297    1.50
Gapped
Lambda     K       H
   0.294   0.110    0.610
Matrix: PAM30
Gap Penalties: Existence: 9, Extension: 1
Number of Sequences: 5031
Number of Hits to DB: 1635
Number of extensions: 77
Number of successful extensions: 77
Number of sequences better than 200000: 49
Number of HSP's better than 200000 without gapping: 0
Number of HSP's gapped: 68
Number of HSP's successfully gapped: 66
Length of query: 16
Length of database: 306907
Length adjustment: 5
Effective length of query: 11
```

```
Effective length of database: 281752
Effective search space: 3099272
Effective search space used: 3099272
T: 11
A: 40
X1: 2 (1.0 bits)
X2: 35 (14.8 bits)
X3: 58 (24.6 bits)
S1: 2 (4.0 bits)
S2: 2 (4.0 bits)
```